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No. of SeqIDs Defined: 4

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<110> APPLICANT: ROEMISCH, JUERGEN
 STOEHR, HANS-ARNOLD
 FEUSSNER, ANNETTE
 LANG, WIEGAND
 WEIMER, THOMAS
 BECKER, MARGRET
 NERLICH, CLAUDIA
 MUTH-NAUMANN, GUDRUN

<120> TITLE OF INVENTION: MUTANTS OF THE FACTOR VII-ACTIVATING PROTEASE AND
 DETECTION METHODS USING SPECIFIC ANTIBODIES

<130> FILE REFERENCE: 06478.1457

<140> CURRENT APPLICATION NUMBER:09912559
 <141> CURRENT FILING DATE:2001-07-26
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 <150> PRIOR APPLICATION NUMBER: DE 100 50 040.4
 <151> PRIOR FILING DATE: 2000-10-10
 <150> PRIOR APPLICATION NUMBER: DE 100 52 319.6
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 <150> PRIOR APPLICATION NUMBER: DE 101 18 706.8
 <151> PRIOR FILING DATE: 2001-04-12
 <160> NUMBER OF SEQ ID NOS: 4
 <170> SOFTWARE: PatentIn Ver. 2.1

<210> SEQ ID NO 1
 <211> LENGTH: 1683
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 1

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<211> LENGTH: 1683

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 2

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<210> SEQ ID NO 3

<211> LENGTH: 560

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 3

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Leu Asp Pro Asp Trp Thr Pro Asp Gln Tyr Asp Tyr Ser Tyr Glu Asp
35 40 45
Tyr Asn Gln Glu Glu Asn Thr Ser Ser Thr Leu Thr His Ala Glu Asn
50 55 60
Pro Asp Trp Tyr Tyr Thr Glu Asp Gln Ala Asp Pro Cys Gln Pro Asn
65 70 75 80
Pro Cys Glu His Gly Gly Asp Cys Leu Val His Gly Ser Thr Phe Thr
85 90 95
Cys Ser Cys Leu Ala Pro Phe Ser Gly Asn Lys Cys Gln Lys Val Gln
100 105 110

Asn	Thr	Cys	Lys	Asp	Asn	Pro	Cys	Gly	Arg	Gly	Gln	Cys	Leu	Ile	Thr	115	120	125
Gln	Ser	Pro	Pro	Tyr	Tyr	Arg	Cys	Val	Cys	Lys	His	Pro	Tyr	Thr	Gly	130	135	140
Pro	Ser	Cys	Ser	Gln	Val	Val	Pro	Val	Cys	Arg	Pro	Asn	Pro	Cys	Gln	145	150	155
Asn	Gly	Ala	Thr	Cys	Ser	Arg	His	Lys	Arg	Arg	Ser	Lys	Phe	Thr	Cys	165	170	175
Ala	Cys	Pro	Asp	Gln	Phe	Lys	Gly	Lys	Phe	Cys	Glu	Ile	Gly	Ser	Asp	180	185	190
Asp	Cys	Tyr	Val	Gly	Asp	Gly	Tyr	Ser	Tyr	Arg	Gly	Lys	Met	Asn	Arg	195	200	205
Thr	Val	Asn	Gln	His	Ala	Cys	Leu	Tyr	Trp	Asn	Ser	His	Leu	Leu	Leu	210	215	220
Gln	Glu	Asn	Tyr	Asn	Met	Phe	Met	Glu	Asp	Ala	Glu	Thr	His	Gly	Ile	225	230	235
Gly	Glu	His	Asn	Phe	Cys	Arg	Asn	Pro	Asp	Ala	Asp	Glu	Lys	Pro	Trp	245	250	255
Cys	Phe	Ile	Lys	Val	Thr	Asn	Asp	Lys	Val	Lys	Trp	Glu	Tyr	Cys	Asp	260	265	270
Val	Ser	Ala	Cys	Ser	Ala	Gln	Asp	Val	Ala	Tyr	Pro	Glu	Glu	Ser	Pro	275	280	285
Thr	Glu	Pro	Ser	Thr	Lys	Leu	Pro	Gly	Phe	Asp	Ser	Cys	Gly	Lys	Thr	290	295	300
Glu	Ile	Ala	Glu	Arg	Lys	Ile	Lys	Arg	Ile	Tyr	Gly	Gly	Phe	Lys	Ser	305	310	315
Thr	Ala	Gly	Lys	His	Pro	Trp	Gln	Ala	Ser	Leu	Gln	Ser	Ser	Leu	Pro	325	330	335
Leu	Thr	Ile	Ser	Met	Pro	Gln	Gly	His	Phe	Cys	Gly	Gly	Ala	Leu	Ile	340	345	350
His	Pro	Cys	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Thr	Asp	Ile	Lys	Thr	355	360	365
Arg	His	Leu	Lys	Val	Val	Leu	Gly	Asp	Gln	Asp	Leu	Lys	Lys	Glu	Glu	370	375	380
Phe	His	Glu	Gln	Ser	Phe	Arg	Val	Glu	Lys	Ile	Phe	Lys	Tyr	Ser	His	385	390	395
Tyr	Asn	Glu	Arg	Asp	Glu	Ile	Pro	His	Asn	Asp	Ile	Ala	Leu	Leu	Lys	405	410	415
Leu	Lys	Pro	Val	Asp	Gly	His	Cys	Ala	Leu	Glu	Ser	Lys	Tyr	Val	Lys	420	425	430
Thr	Val	Cys	Leu	Pro	Asp	Gly	Ser	Phe	Pro	Ser	Gly	Ser	Glu	Cys	His	435	440	445
Ile	Ser	Gly	Trp	Gly	Val	Thr	Glu	Thr	Gly	Lys	Gly	Ser	Arg	Gln	Leu	450	455	460
Leu	Asp	Ala	Lys	Val	Lys	Leu	Ile	Ala	Asn	Thr	Leu	Cys	Asn	Ser	Arg	465	470	475
Gln	Leu	Tyr	Asp	His	Met	Ile	Asp	Asp	Ser	Met	Ile	Cys	Ala	Gly	Asn	485	490	495
Leu	Gln	Lys	Pro	Gly	Gln	Asp	Thr	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	500	505	510
Leu	Thr	Cys	Glu	Lys	Asp	Gly	Thr	Tyr	Tyr	Val	Tyr	Gly	Ile	Val	Ser	515	520	525
Trp	Gly	Leu	Glu	Cys	Gly	Lys	Arg	Pro	Gly	Val	Tyr	Thr	Gln	Val	Thr	530	535	540
Lys	Phe	Leu	Asn	Trp	Ile	Lys	Ala	Thr	Ile	Lys	Ser	Glu	Ser	Gly	Phe	545	550	555
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<210> SEQ ID NO 4

<211> LENGTH: 560

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 4

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Leu Asp Pro Asp Trp Thr Pro Asp Gln Tyr Asp Tyr Ser Tyr Glu Asp
          35           40           45
Tyr Asn Gln Glu Glu Asn Thr Ser Ser Thr Leu Thr His Ala Glu Asn
          50           55           60
Pro Asp Trp Tyr Tyr Thr Glu Asp Gln Ala Asp Pro Cys Gln Pro Asn
          65           70           75           80
Pro Cys Glu His Gly Gly Asp Cys Leu Val His Gly Ser Thr Phe Thr
          85           90           95
Cys Ser Cys Leu Ala Pro Phe Ser Gly Asn Lys Cys Gln Lys Val Gln
          100          105          110
Asn Thr Cys Lys Asp Asn Pro Cys Gly Arg Gly Gln Cys Leu Ile Thr
          115          120          125
Gln Ser Pro Pro Tyr Tyr Arg Cys Val Cys Lys His Pro Tyr Thr Gly
          130          135          140
Pro Ser Cys Ser Gln Val Val Pro Val Cys Arg Pro Asn Pro Cys Gln
          145          150          155          160
Asn Gly Ala Thr Cys Ser Arg His Lys Arg Arg Ser Lys Phe Thr Cys
          165          170          175
Ala Cys Pro Asp Gln Phe Lys Gly Lys Phe Cys Glu Ile Gly Ser Asp
          180          185          190
Asp Cys Tyr Val Gly Asp Gly Tyr Ser Tyr Arg Gly Lys Met Asn Arg
          195          200          205
Thr Val Asn Gln His Ala Cys Leu Tyr Trp Asn Ser His Leu Leu Leu
          210          215          220
Gln Glu Asn Tyr Asn Met Phe Met Glu Asp Ala Glu Thr His Gly Ile
          225          230          235          240
Gly Glu His Asn Phe Cys Arg Asn Pro Asp Ala Asp Glu Lys Pro Trp
          245          250          255
Cys Phe Ile Lys Val Thr Asn Asp Lys Val Lys Trp Glu Tyr Cys Asp
          260          265          270
Val Ser Ala Cys Ser Ala Gln Asp Val Ala Tyr Pro Glu Glu Ser Pro
          275          280          285
Thr Glu Pro Ser Thr Lys Leu Pro Gly Phe Asp Ser Cys Gly Lys Thr
          290          295          300
Glu Ile Ala Glu Arg Lys Ile Lys Arg Ile Tyr Gly Gly Phe Lys Ser
          305          310          315          320
Thr Ala Gly Lys His Pro Trp Gln Ala Ser Leu Gln Ser Ser Leu Pro
          325          330          335
Leu Thr Ile Ser Met Pro Gln Gly His Phe Cys Gly Gly Ala Leu Ile
          340          345          350
His Pro Cys Trp Val Leu Thr Ala Ala His Cys Thr Asp Ile Lys Thr
          355          360          365
Arg His Leu Lys Val Val Leu Gly Asp Gln Asp Leu Lys Lys Glu Glu
          370          375          380
Phe His Glu Gln Ser Phe Arg Val Gln Lys Ile Phe Lys Tyr Ser His
          385          390          395          400
Tyr Asn Glu Arg Asp Glu Ile Pro His Asn Asp Ile Ala Leu Leu Lys
          405          410          415
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		435					440					445					
Ile	Ser	Gly	Trp	Gly	Val	Thr	Glu	Thr	Gly	Lys	Gly	Ser	Arg	Gln	Leu		
	450					455					460						
Leu	Asp	Ala	Lys	Val	Lys	Leu	Ile	Ala	Asn	Thr	Leu	Cys	Asn	Ser	Arg		
465					470					475					480		
Gln	Leu	Tyr	Asp	His	Met	Ile	Asp	Asp	Ser	Met	Ile	Cys	Ala	Gly	Asn		
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Trp	Gly	Leu	Glu	Cys	Glu	Lys	Arg	Pro	Gly	Val	Tyr	Thr	Gln	Val	Thr		
	530					535					540						
Lys	Phe	Leu	Asn	Trp	Ile	Lys	Ala	Thr	Ile	Lys	Ser	Glu	Ser	Gly	Phe		
545					550					555					560		